

1. *Chrysomelidae* (10 species)
 2. *Curculionidae* (10 species)
 3. *Chrysomelidae* (10 species)
 4. *Curculionidae* (10 species)
 5. *Chrysomelidae* (10 species)
 6. *Curculionidae* (10 species)
 7. *Chrysomelidae* (10 species)
 8. *Curculionidae* (10 species)
 9. *Chrysomelidae* (10 species)
 10. *Curculionidae* (10 species)

Type II Transmembrane domain:
amino acids 32-57

FIGURE 226

GCCCCGCCCTCCGCCCTCCGCACTCCCGCCTCCCTCCCTCCGCCCGCTCCCGCGCCCTCCTCCCTCCCTCCTCCC
CAGCTGTCCCCTTCGCGTCATGCCGAGCCTCCCGCCCCCGGCCCGCCGCTGCTGCTCCTCGGGCTGCTGCTGCT
CGGCTCCCAGCCCGCCCGCGCGCCGAGAGCCCCCGCTGCTGCCATCCGTTCTGAGAAGGAGCCGCTGCC
CGTTCCGGGAGCGGCAGGTAGGTGGGCGCCCGGGGAGGCGCGGGCGGGGAGTCCGGCTCGGGGCGAGTCAGCGC
CAGCCCCGAGGGGGCGCGGGGCGCAGGTGGCTCGGCGCGGGCGGGCGGCCGAGGGTGGGCGGGGCGAGAAGGGC
GCGGTGCCTGGGACCCGGGACCCGCGGGCAGCCCCCGGGCGGCACACGGCGGAGCTGGGCAGCGGCCTCCAGC
CAAGCCCGTCCCCGAGGCTGCACCTTCGGCGGGAGGTCTATGCCTTGGACGAGACGTGGCACCCGACCTAGG
GGAGCCATTCCGGGTGATGCGCTGCGTGTGTGCGCCTGCGAGGCGCAGTGGGGTCCCGTACCAGGGGCCCTGG
CAGGGTCAGCTGCAAGAACATCAAACAGAGTGCACCCAGGCTGTGGGCAGCCGCGCCAGCTGCCGGGACA
CTGCTGCCAGACCTGCCCCAGGACTTCGTGGCGCTGCTGACAGGGCCGAGGTCCGAGGCGGTGGCACAGGCCG
AGTCTCGCTGCTGCGCTCTAGCCTCCGCTTCTCTATCTCTACAGGCGGCTGGACCGCCCTACCAGGATCCGCTT
CTCAGACTCCAATGGCAGTGTCTGTTTGGACACCTGCAGCCCCACCAAGATGGCCTGGTCTGTGGGGTGTG
GCGGGCAGTGCCTCGGTTGTCTCTGCGGCTCCTTAGGGCAGAACAGCTGCATGTGGCACTTGTGACACTCACTCA
CCCTTCAGGGGAGGTCTGGGGGCTCTCATCCGGCACCGGGCCCTGTCCCCAGAGACCTTCAGTGCCATCCTGAC
TCTAGAAGGCCCCCACCAGCAGGGCGTAGGGGGCATCACCTGTCTACTCTCAGTGACACAGAGGACTCCTTGCA
TTTTTTGCTGCTCTTCCGAGGCCCTTGACAGGACTTAACCCAGGTTCCCTTGAGGCTCCAGATTCTACACAGGGGCA
GCTACTGCGAGAACTTCAGGCCAATGTCTCAGCCAGGAACAGGCTTTGCTGAGGTGCTGCCAACCTGACAGT
CCAGGAGATGGACTGGCTGGTGTGCGGGGAGCTGCAGATGGCCCTGGAGTGGGCAGGCAGGCCAGGGCTGCGCAT
CAGTGACACATTGCTGCCAGGAAGAGCTGCGACGTCTGCAAGTGTCTTTGTGGGGCTAATGCCCTGATCCC
AGTCCAAACGGGTGCTGCCGGCTCAGCCAGCCTCACTCTGCTAGGAAATGGCNCCTGATCCTCCAGGTGCAATT
GGTAGGGACAACCGGATGGTGGTGCATGACACTGGAACCAAGCCTCAGCGGAGGGATCAGCCACTGTCTCT
GTGCCACATGGCTGGCCTATCCTCCCTGCCCCAGGCCGTGGGTATCTGCCCTGGGCTGGGGTGCCCGAGGGGC
TCATATGCTGCTGCAGAAATGAGCTCTTCTGAACGTGGGCACCAAGGACTTCCAGACGGAGAGCTTCGGGGGCA
ACGTGGCTGCCCTGCCCTACTGTGGGGCATAGCGCCCGCCCTGCCCGTCCCCCTAGCAGGAGCCCTGGTGTACC
CCCTGTGAAGAGCCAAGCAGCAGGGCACGCCTGGCTTTCTTGGATACCCACTGTCACTGCACTATGAAGTGCT
GCTGGCTGGGCTTGGTGGCTCAGAACAGGCACTGTCACTGCCACCTCCTTGGGCCTCCTGGAACGCCAGGGCC
TCGGCGGCTGCTGAAGGGATTCTATGGCTCAGAGGCCCAGGGTGTGGTGAAGGACCTGGAGCCGGAAGTGTGCG
GCACCTGGCAAAAGGCATGGCTTCCCTGATGATCACCACCAAGGTAGCCCCAGAGGGGAGCTCCGAGGGCAGCCT
CTCCTCCCAGGTGCACATAGCCAACCAATGTGAGGTGGCGGACTGCGCCTGGAGGCGGCCGGGGCCGAGGGGGT
GCGGGCGCTGGGGGCTCCGGATACAGCCTCTGCTGCGCCGCTGTGGTGCCTGGTCTCCCGGCCCTAGCGCCCGC
CAAACCTGGTGGTCTTGGGCGGCCCGAGACCCCAACATGCTTCTTCGAGGGGCGAGCAGCGCCCCACGGGGC
TCGCTGGGCGCCCAACTACGACCCGCTCTGCTCACTTGCCAGAGACGAACGGTGATCTGTGACCCGGT
GGTGTGCCACCCAGCTGTGTGCACTGACCTGTTTGAAGAAATACTGGCCTTTCTGGGACCAAGGCAGGGATGCTT
TTTTGATGGTGACCGAGCTGGCGGGCAGCGGTACCGGTTGGCACCCCGTTGTGCCCTTTGGCTTAATTA
GTGTGCTGTCTGCACCTGCAAGCAGGGGGGCACTGGAGAGGTGCACTGTGAGAAGGTGAGTGTCCCGGCTGGC
CTGTGCCCAGCCTGTGCGTGTCAACCCACCGACTGTGCAACAGTGTCCAGGTGAGGCCACCCACAGCTGGG
GGACCCCATGACGGCTGATGGGCCCCGGGGCTGCCGTTTGTGGGCAGTGGTTCACAGAGAGTCAAGAGCTGGCA
CCCCCTAGTGCCCCGTTTGGAGAGATGAGCTGTATCACTGCAGATGTGGGGTAAGTGGGGAGCAGAGGCTTGT
GTGAGGTGGGTACTGGGAGCCTGGTCTGGAGTAGGGAGACTTCCAGGGAGGTCCCTGAAGAAGTGAAGGTCA
CTGTGTCCAGTGCCTCTGGGGGACACTCAGTGTCTGCTCTGTCTTGTACAGGCAGGGGTGCCTCACTGTGAGC
GGGATGACTGTTCACTGCCACTGTCTGTGGCTCGGGGAAGGAGAGTGCATGCTGTTCCCGCTGCACGGCCACC
GGCGGCGTAAGTGAGGGAGTCCAGGGTCAGCAGCTGTGAGTGGAGGGCTCACCTGCCTGTGGGACTCCTGATCAG
GGAAGGGAGCACTCACTGTGTGCAGGAACAGTGCAGCCTGCCTCACAAGTGCCATTCCAATCCACCCTCACAGCA
ACCTGGTGGAATTGTTATTTATGACCTTTCTTTACAAATGAGATTTCTGAAGCTCAGAGAAATTAAGCAACGAG
ATGAAGGTACCCAGCTGTGTGCACTGACCTGTTTGAAGAAATACTGGCCTTTCTGGGACCAAGGCAGGGATGCTT
TGCCCTGCCCTCTATGCCTCTCTGTGCCTCTCCACTCCCTCTCCCTCCTCCAACATTCCCTCCCTTCTGTCTCC
AGCAGCCCCAGAGACCAGAACTGATCCAGAGCTGGAGAAAGAAGCCGAAGGCTCTTAGGGAGCAGCCAGAGGGCC
AAGTGACCAAGAGGATGGGGCCTGAGCTGGGGAAGGGGTGGCATCGAGGACCTTCTTGCACTTCTCTGTGGGAAG
CCCAGTGCCTTTGCTCCTCTGTCTGCTCTACTCCACCCCCACTACCTCTGGGAACCAAGCTCCACAAGGGG
GAGAGGCAGCTGGGCCAGACCGAGGTCAAGCCACTCCAAGTCTGCCCTGCCACCCTCGGCCTCTGTCTGGAA
GCCCCACCCCTTTCTTCTGTACATAATGTCACTGGCTTGTGGGATTTTAAATTTATCTTCACTCAGCACCAG
GGCCCCGACACTCCACTCCTGTGCCCTGAGCTGAGCAGAGTCAATTATTGGAGAGTTTTGTATTTATTAAC
ATTTCTTTTTTCACTCTTTGGGCATGAGGTGGCTCTTTGTGGCCAGGAACCTGAGTGGGGCTGGTGGAGAAGGG
GCNAGAGTAGGAGGTGAGAGAGAGGAGCTCTGACACTTGGGGAGCTGAAAGAGACCTGGAGAGGCAGAGGATAG
CGTGGCCTTTGGCTGGCATNCTGGGTTCCGCGAGAGGGGTGGGGATGGTTCTTGAGATGGTCTAGAGACTCAAG
AATTTAGGAAGTAGAAGCAGGATTTGACTCAAGTTTAGTTTCCACATCGCTGGCCTGTTTGTGACTTCACTG
TTTGAAGTTGCTCCAGAGAGAGAATCAAGGTGTCAACAGGCCCTCTCTCCCTCCTTCCCTTCCCTTTCTCT
TTCCCTCCCCCTCCCCCTCCCCCTCCCCCTCCCCCTCC

FIGURE 227

GGCCGAGCGGGGTGCTGCGCGGCGGCCGTGATGGCTGGTGACGGCGGGGCCGGGCAGGGGA
CCGGGGCCGCGGCCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGAATCACCGCCTGGCCCGAC
TCCACCATGAACGTCGCGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAGAAGGG
GACAAGACAGCTGTTAGGCTCACGCACGCAGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTAC
TGCTGGCTGCACTGCTTCTGGGCTGCCTTGTGGCCCTAGGGGTCCAGTACCACAGAGACCCA
TCCCACAGCACCTGCCTTACAGAGGCCTGCATTTCGAGTGGCTGGAAAAATCCTGGAGTCCCT
GGACCGAGGGGTGAGCCCCTGTGAGGACTTTTACCAGTTCTCCTGTGGGGGCTGGATTTCGA
GGAACCCCCTGCCCGATGGGCGTTCTCGCTGGAACACCTTCAACAGCCTCTGGGACCAAAC
CAGGCCATACTGAAGCACCTGCTTGAAAACACCACCTTCAACTCCAGCAGTGAAGCTGAGCA
GAAGACACAGCGCTTCTACCTATCTTGCCTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCC
AGCCACTGAGAGACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACCAG
GACAACTTTATGGAGGTGTTGAAGGCAGTAGCAGGGACCTACAGGGCCACCCATTCTTCAC
CGTCTACATCAGTGCCGACTCTAAGAGTTCCAACAGCAATGTTATCCAGGTGGACCAGTCTG
GGCTCTTTCTGCCCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAGAAAGTAAGGAAC
ATCTTCCGAACCCCCATCCCTACCCCTGGCTGAGCTGGGCTGATCCCTGTTGACTTTTCCCT
TTGCCAAGGGTCAGAGCAGGGAAGGTGAGCCTATCCTGTCACCTAGTGAACAACTGCCCCCT
CCTTTCTTTCTTCTTTTCTTCCCTCCCTCCCTTTTCTTCCCCTTTTCTTCCCTTCCCTTCC
TCTTATTCTTCTAGTAGGTTTCATAGACACCTACTGTGTGCCAGGTCCAGTGGGGGAATTTCG
GAGATATAAGTTTCCGAGCCATTGCCACAGGAAGCGTTCAGTGTCGATGGGTTTCATGGACCT
AGATAGGCTGATAACAAAGCTCACAAGAGGGTCCTGAGGATTTCAGGAGAGACTTATGGAGCC
AGCAAAGTCTTCCCTGAAGAGATTGCATTTGAGCCAGGTCCTGTAG